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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated nucleic acid molecule comprising a MADS box, which is capable of altering the flowering time  
5 of a plant, and which comprises
  - (a) the nucleotide sequence set out in any one of SEQ ID NOS. 1, 2, 4, and 6 to 15;
  - (b) a nucleic acid molecule capable of hybridizing  
10 to a sequence set out in (a), other than to the MADS box region thereof, under at least low stringency hybridization conditions; or
  - (c) a nucleic acid molecule which has at least 70% sequence identity, outside the MADS box region, with a sequence set out in (a).
- 15 2. A nucleic acid molecule according to Claim 1, in which the nucleic acid molecule is
  - (a) capable of hybridizing to a nucleotide sequence as set out in any one of SEQ ID NOS: 1, 2, 4,  
20 and 6 to 15 under high stringency hybridization conditions; or
  - (b) has at least 80% sequence identity with a sequence set out in Claim 1 (a).
3. An isolated nucleic acid molecule according to Claim 1, in which expression of the nucleic acid molecule  
25 in the plant, in the sense orientation under the control of a promoter sequence, is capable of delaying the flowering of the plant.
4. An isolated nucleic acid molecule according to Claim 1, which is capable of accelerating the flowering of  
30 a plant.
5. An isolated nucleic acid molecule according to Claim 4, in which expression of the nucleic acid molecule in the plant in the anti-sense orientation under the control of a promoter sequence is capable of accelerating  
35 the flowering of the plant.
6. An isolated nucleic acid molecule according to Claim 1, which comprises a nucleotide sequence

corresponding to a *FLOWERING LOCUS F (FLF)* gene, or a PCR primer or a biologically active fragment derived therefrom.

7. A vector comprising a nucleic acid molecule according to Claim 1.
8. A plant cell transformed with a nucleic acid according to Claim 1.
9. A plant transformed with a nucleic acid molecule according to Claim 1.
10. A method of isolating a nucleic acid molecule capable of altering the flowering time of a target plant, comprising the step of using a nucleic acid molecule according to Claim 1, or a functional portion thereof, as a hybridisation probe or polymerase chain reaction (PCR) primer, and optionally detecting hybridisation.
11. A method according to Claim 10, in which the nucleic acid molecule is capable of hybridizing to a nucleotide sequence as set out in any one of SEQ ID NOS: 1, 2, 4, and 6 to 15 under at least low stringency hybridization conditions, and the nucleic acid molecule does not include of MADS box region.
12. A method of delaying flowering in a plant, comprising the step of introducing a nucleic acid molecule according to Claims 1 into cells of the plant, optionally such that expression of the nucleic acid molecule is under the control of an inducible promoter, and over-expressing the nucleic acid molecule.
13. A method of inducing early flowering in a plant, comprising the step of reducing the degree of expression of a nucleic acid molecule according to Claim 1 in the plant.
14. A method of modifying the vegetative and/or floral phenotype of a plant, comprising the step of increasing the level of expression of a *FLF* gene, thereby to modify the level of production or activity of a gibberellin in the plant.
15. A method of modifying the response of a plant to

vernalisation, comprising the step of increasing or decreasing the level of expression of an *FLF* gene.

16. A method according to Claim 14, in which the *FLF* gene comprises a nucleic acid molecule according to Claim

5 1.

17. A polypeptide encoded by a nucleic acid molecule according to Claim 1.

18. An *FLF* polypeptide, comprising the amino acid sequence set out in any one of SEQ ID NOS: 3, 5, and 16 to  
10 30, or having at least 70% sequence identity thereto.

19. An antibody directed against a polypeptide according to Claim 17.

20. A method of assaying the level of expression of *FLF* polypeptide, comprising the step of using an antibody  
15 according to Claim 19.

21. A method of selecting plants with low or high levels of expression of *FLF*, comprising the step of determining the level of *FLF* mRNA or *FLF* polypeptide in the plant.

20 22. A method according to Claim 20, in which the plants are members of a naturally-occurring population.